

*Amendments to the Claims*

1-77. (Cancelled)

78. (Currently Amended) A method of introgressing an allele ~~conferring soybean cyst nematode resistance~~ into a ~~non-resistant~~ soybean plant comprising

(A) crossing at least one SCN resistant soybean plant having an rhg1 SCN resistant allele with at least one SCN sensitive soybean plant having an rhg1 SCN sensitive allele in order to form a segregating population, ~~wherein said at least one SCN resistant soybean plant having said rhg1 SCN resistant allele is selected from the group consisting of PI200499, A2869, PI404198 B, PI404166, PI548988, PI507354, PI84751, PI407922, AG4301, and SCN resistant progeny thereof,~~

(B) screening said segregating population with one or more nucleic acid markers to ~~identify an rhg1 SCN resistant allele~~ determine if one or more soybean plants from said segregating population contains a deletion of 19 nucleotides corresponding to position 48881 of SEQ ID NO: 2, and

(C) selecting, if present, one or more members soybean plants of said segregating population ~~having said rhg1 SCN resistant allele~~ containing said deletion.

79. (Currently Amended) The method according to claim 78, wherein said one or more members of said segregating population have a yellow soybeans soybean seed.

80.-85. (Cancelled)

86. (Currently Amended) A method of introgressing an allele ~~conferring soybean cyst nematode resistance~~ from a first soybean plant comprising a polymorphism relative to a second soybean plant into a ~~non-resistant~~ selected soybean plant comprising screening with one or more nucleic acid markers a population of soybean plants formed by a cross of said first and said second soybean plant and selecting a soybean plant, wherein said allele is an ~~rhg1~~ allele having

one or more polymorphisms in a protein coding region corresponding to nucleotides 45163 to 45314, 45450 to 45509, 46941 to 48763 or 48975 to 49573 of SEQ ID NO: 2, wherein said one or more nucleic acid markers are capable of detecting one or more single nucleotide polymorphisms, and wherein said selected soybean plant is SCN resistant,

thereby introgressing said allele from said first soybean plant comprising a polymorphism into said ~~non-resistant~~ selected soybean plant.

87. (Currently Amended) The method according to claim 86, wherein said ~~single nucleotide~~ polymorphisms ~~in said rhg1 gene~~ are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, ~~47057~~, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316 of SEQ ID NO: 2.

88. (Currently Amended) The method according to claim 86, wherein said introgressing said allele into said ~~non-resistant~~ selected soybean plant results in ~~one or more resistant progeny~~ having a yellow soybeans soybean seed.

89. (Currently Amended) A method of introgressing an allele ~~conferring soybean cyst nematode resistance~~ comprising a polymorphism into a ~~non-resistant~~ soybean plant lacking said polymorphism comprising screening a population of soybean plants with one or more nucleic acid markers and selecting a soybean plant, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, ~~46227, 46703, 47057, 47057~~, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, ~~48881~~, and 49316, ~~and wherein said selected soybean plant is SCN resistant,~~

thereby ~~introgressing said allele into said non-resistant~~ selecting a soybean plant comprising said polymorphism.

90. (Currently Amended) The method according to claim 89, wherein said introgressing said allele comprising a polymorphism into said ~~non-resistant~~ soybean plant results in one or more ~~resistant progeny~~ soybean plant having a yellow soybeans soybean seed and said polymorphism.

91. (Currently Amended) A method of introgressing an rhg1 SCN resistant allele ~~confering~~ soybean cyst nematode resistance into a non-resistant soybean plant comprising

(A) crossing at least one SCN resistant soybean plant having an said rhg1 SCN resistant allele corresponding to an rhg1 SCN resistant allele present in Peking with at least one SCN sensitive soybean plant having an rhg1 SCN sensitive allele in order to form a segregating population, ~~wherein said at least one SCN resistant soybean plant having said rhg1 SCN resistant allele is selected from the group consisting of PI200499, A2869, PI404198 B, PI404166, PI548988, PI507354, PI84751, PI407922, AG4301, and SCN resistant progeny thereof having an rhg1 SCN resistant allele from PI200499, A2869, PI404198 B, PI404166, PI548988, PI507354, PI84751, PI407922, and AG4301,~~

(B) screening said segregating population with one or more nucleic acid markers to identify an said rhg1 SCN resistant allele, wherein said one or more nucleic acid markers are capable of detecting a polymorphism located at corresponding to a position in SEQ ID NO: 2 between 45163 and 49573, and

(C) selecting one or more members of said segregating population having said rhg1 SCN resistant allele.

92. (Currently Amended) The method according to claim 91, wherein said one or more members of said segregating population have a yellow soybeans soybean seed.

93. (Currently Amended) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting a single nucleotide ~~polymorphisms~~ polymorphism or INDEL ~~mutations~~ mutation.

94. (Currently Amended) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, ~~45400, 45416, 45439,~~ 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, 49316, ~~46227,~~ and 46703, ~~and 48881.~~

95. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms.

96. (Currently Amended) The method according to claim 95, wherein said single nucleotide polymorphisms are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, ~~45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057,~~ 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

97. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting INDEL mutations.

98.-106. (Cancelled)